

Best Local Similarity 92.04, Evid. NO. 574111
 Matches 29, Score 111.1, Positives 11, Index 0.248, 0
 QY 2 DQILLMDGPPKHLVDPLQSS 26
 DB 469 DQILLMDGPPKHLVDPLQSS 463

RESULT 4
 CEIT_MESAU STANDARD, FNT, 263 AA.
 ID CEIT_MESAU
 AC F00931
 DT 01-MAY-1992 (Rel. 35, Created)
 DT 01-MAY-1992 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CHOLESTERYL ESTER TRANSFER PROTEIN (LIPID TRANSFER PROTEIN 1)
 DE (FRAGMENT)
 DE CEIT.
 OS Mesocricetus auratus (Golden hamster).
 CC Eukaryota; Metazoa; Chordata; Rodentia; Volelata; Muridae.
 CC Eutheria; Rodentia; Sciuroidea; Muridae; Muridae; Mesocricetus
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91154277.
 PA TANG X C, MONTIN P, GUTIERREZ E, GUTIERREZ I, YACOB L M
 ACILLIN E, SCHNITZER-PELCOFF R, TALL A R.
 RT "Hammerhead ribbons, ribbons and ribbons are major sources of lipid
 RT transfer proteins (MESA).
 RL J Biol Chem 266:14911-14914(1991)
 CC
 CC FUNCTION: CEIT IS AN EXTREMELY HIGHLY SPECIFIC LIPID TRANSFER
 CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSFER
 CC OF CHOLESTEROL
 CC SUBCELLULAR LOCATION: EXTRACELLULAR
 CC
 CC TISSUE SPECIFICITY: PLASMA.
 CC
 CC SIMILARITY: HIGHLY TO THE SCINOTRIPPELIPID FAMILY
 CC
 CC THIS SWISS-PROT entry is obsolete. It is produced through a collaboration
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Query Match 83.84, Evid. NO. 1, Length 289
 Best Local Similarity 80.04, Evid. NO. 2, Length 289
 Matches 29, Score 111.1, Positives 11, Index 0.248, 0
 QY 2 DQILLMDGPPKHLVDPLQSS 26
 DB 265 DQILLMDGPPKHLVDPLQSS 289

RESULT 5
 YDAG_HAFIN STANDARD, PRT, 313 AA
 ID YDAG_HAFIN
 AC Q57184: Q05059:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN H1371.1.
 DE H1371.1
 OS Haemophilus influenzae

QY 12 GPPHLLVDPLQSS 25
 DB 86 GPPHLLVDPLQSS 99

RESULT 6
 YDAG_HAFIN STANDARD, PRT, 313 AA.
 ID YDAG_HAFIN
 AC P76055: Q47568:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN H1371.1.
 DE H1371.1
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subphylum; Enterobacteriaceae
 CC Escherichia.
 CC
 CC SEQUENCE FROM N.A.
 CC STAIN-612 / M6155:
 CC MEDLINE: 97426617.
 CC BLATTNER F R, PLUNKETT G, III, RUCH C A, PERA N T, ROSS J V,
 CC PETER M, GOLLADE-VIDOS J, GRASMAN P R, WATKINS J, WATKINS G F,
 CC GREGOR J, DAVIS N, KIRKPATRICK H A, GREEN M A, ROSE D C,
 CC MAU R, SHAO Y.
 CC "The complete genome sequence of Escherichia coli K-12."
 CC Science 277:1232-1238(1997).
 CC
 CC SEQUENCE OF 1.40 FROM N.A.
 CC STAIN-612 / M6155:
 CC

Query Match 85.84, Evid. NO. 1, Length 289
 Best Local Similarity 80.04, Evid. NO. 2, Length 289
 Matches 29, Score 111.1, Positives 11, Index 0.248, 0
 QY 12 GPPHLLVDPLQSS 25
 DB 86 GPPHLLVDPLQSS 99

[illegible]

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CC FMBL: X75941: CAA53535.1: -
DK

